

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/570,121  
Source: IFWP  
Date Processed by STIC: 11/17/2006

***ENTERED***



IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/570,121

DATE: 11/17/2006  
TIME: 08:38:11

Input Set : F:\ARS-125-SEQ LIST.txt  
Output Set: N:\CRF4\11172006\J570121.raw

3 <110> APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
5 <120> TITLE OF INVENTION: NOVEL UBP8rp POLYPEPTIDES AND THEIR USE IN THE TREATMENT OF  
PSORIASIS  
7 <130> FILE REFERENCE: WO 886  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/570,121  
C--> 9 <141> CURRENT FILING DATE: 2006-02-28  
9 <160> NUMBER OF SEQ ID NOS: 79  
11 <170> SOFTWARE: PatentIn version 3.1  
13 <210> SEQ ID NO: 1  
14 <211> LENGTH: 7260  
15 <212> TYPE: DNA  
16 <213> ORGANISM: Homo sapiens  
18 <220> FEATURE:  
19 <221> NAME/KEY: exon  
20 <222> LOCATION: (851)..(1017)  
21 <223> OTHER INFORMATION: exon 1  
24 <220> FEATURE:  
25 <221> NAME/KEY: Intron  
26 <222> LOCATION: (1018)..(1046)  
27 <223> OTHER INFORMATION:  
29 <220> FEATURE:  
30 <221> NAME/KEY: exon  
31 <222> LOCATION: (1047)..(1675)  
32 <223> OTHER INFORMATION: exon 2  
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37 <222> LOCATION: (1676)..(1718)  
38 <223> OTHER INFORMATION:  
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41 <221> NAME/KEY: exon  
42 <222> LOCATION: (1719)..(2371)  
43 <223> OTHER INFORMATION: exon 3  
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49 tcattcattt ttgttgcgtga gcagctgccg agtattgtt gaatcccagt ttattcattt 120  
51 gtttctgtgt ctccagggttga tagacatgtt gattcctcca gttagggtt gttatataatg 180  
53 aagccactat aaataactgc ttacaagtgt ggacttacat ttttatttct tttggataaaa 240  
55 tacgtatattt tggaattgtt gggccatgtt gtaatagatg ggtaactgtt taagaaaactt 300  
57 ccataccact ttacaaaattt gctgccacat tttttgcatt cctaccagca atatcagaca 360  
59 ttccatattt ttccatattt ttgcgtgtt taagacttat catatgtt tttaactttt 420  
61 tctgtcttag gtgtatgtt atggtttctt attgtgttta taacttgac ttctttgtt 480  
63 actagtattt tttgttatct tttcatgtt atctaagcga cttattacat atatttatg 540  
65 aactattttgc caaattcaat gattaattcc agagactttt tcagaattcc ctatgtttt 600  
67 ctacatatac aatgaagttt gtagacaaaga aagactttca tttcttcctt tcttatccat 660

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Input Set : F:\ARS-125-SEQ LIST.txt  
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71	tggctcaaa	ctcctgatct	caagtgatcc	tcccacctca	gcctcccaa	atgcaggat	780
73	tacaggcatg	agccaccatg	cctggccctt	gttgcactgg	ttaggatgac	tgttaggtgt	840
75	ttaaacaaga	atg atg aga	gct cac atg	ttt gtt tac	aag gaa ctt	aaa	889
76	Met Met Arg	Ala His Met	Phe Val Tyr	Lys Glu	Leu Lys		
77	1	5	10				
79	caa att tac	aag aaa aaa	acc cat ccc	cat caa aaa	gtg ggc	aaa gga	937
80	Gln Ile Tyr	Lys Lys Lys	Thr His Pro	His Gln Lys	Val Gly	Lys Gly	
81	15	20	25				
83	tat aaa cag aca	ctt ctc aga	gga aga cat	tta cgt	ggc caa	gaa aca	985
84	Tyr Lys Gln	Thr Leu Leu	Arg Gly Arg	His Leu Arg	Gly Gln	Glu Thr	
85	30	35	40	45			
87	tat gaa aaa aag	ctc aca cac	gta tat gaa	ac gtgactgttt	ataatccatat		1037
88	Tyr Glu Lys	Lys Leu Thr	His Val Tyr	Glu Thr			
89	50	55					
91	ccaaaaaaag	a act gat ttc	aag caa cag	cag tat tac	ttc cat tca	ata	1086
92	Thr Asp Phe	Lys Gln Gln	Tyr Tyr Phe	His Ser Ile			
93	60	65					
95	ctt gga cct	gca aac atc	aaa aaa gcc	act gga	gaa act gaa	cga ctc	1134
96	Leu Gly Pro	Ala Asn Ile	Lys Lys Ala	Thr Gly	Glu Thr	Glu Arg Leu	
97	70	75	80	85			
99	tct gaa agc	ctt aaa cta	aga tat gaa	gaa gtt	gaa atc	tgg aaa aaa	1182
100	Ser Glu Ser	Leu Lys Leu	Arg Tyr Glu	Glu Val Glu	Ile Trp	Lys Lys	
101	90	95	100				
103	ctt gag gaa	aag gac agg	cag ggg gaa	gca cag	tgg cta	caa caa aaa	1230
104	Leu Glu Glu	Asp Arg Gln	Gly Glu Ala	Gln Trp Leu	Gln Gln	Lys	
105	105	110	115				
107	agg cag gaa	aca gga	aga gag	gat ggc	agc atg	ttg gct	1278
108	Arg Gln Glu	Thr Gly Arg	Glu Asp Gly	Ser Met	Leu Ala	Lys Gly Ser	
109	120	125	130				
111	ttg gag att	gta ttg gat	tcc aaa gac	aaa acc	caa aag	agc aat ggt	1326
112	Leu Glu Ile	Val Leu Asp	Ser Lys Asp	Lys Thr	Gln Lys	Ser Asn Gly	
113	135	140	145				
115	gaa aag aat	gaa aaa tgt	gag acc aaa	gag aaa	gga gca	atc aca gca	1374
116	Glu Lys Asn	Glu Lys Cys	Glu Thr Lys	Glu Lys Gly	Ala Ile	Thr Ala	
117	150	155	160	165			
119	aag gaa cta	tac aca atg	atg atg gat	aaa aac	atc agc	ttg att ata	1422
120	Lys Glu Leu	Tyr Thr Met	Met Met Asp	Lys Asn Ile	Ser Leu	Ile Ile	
121	170	175	180				
123	atg gat gct	caa aga atg	cag gat tat	cag gat	tcc tgt	att tta cat	1470
124	Met Asp Ala	Gln Arg Met	Gln Asp Tyr	Gln Asp Ser	Cys Ile	Leu His	
125	185	190	195				
127	tct ctc agt	gtt cct gaa	aaa gcc	atc agt	cca gga	gtc act gct	1518
128	Ser Leu Ser	Val Pro Glu	Lys Ala Ile	Ser Pro	Gly Val	Thr Ala Ser	
129	200	205	210				
131	tgg att gaa	gca cac ctc	cca gat	gat tct	ata gat	aca tgg aag aag	1566
132	Trp Ile Glu	Ala His Leu	Pro Asp Asp	Ser Ile Asp	Thr Trp	Lys Lys	
133	215	220	225				
135	agg ggg aat	gtg gag tat	atg gta	ctt ctt	gac tgg	ttt agt tct	1614

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136	Arg	Gly	Asn	Val	Glu	Tyr	Met	Val	Leu	Leu	Asp	Trp	Phe	Ser	Ser	Ala	
137	230				235				240							245	
139	aaa	gat	tta	cag	att	gga	aca	aca	ctc	tgg	cat	ctg	aaa	gat	gca	ctt	1662
140	Lys	Asp	Leu	Gln	Ile	Gly	Thr	Thr	Leu	Trp	His	Leu	Lys	Asp	Ala	Leu	
141					250				255							260	
143	ttc	aag	tgg	gaa	a	gtaaaaactgt	cctgtgcaat	gggccttggg	cctttgggtt	tag							1718
144	Phe	Lys	Trp	Glu													
145					265												
147	ag	gga	ggc	tat	aaa	aac	tgg	ttc	ctt	tgc	tat	tcc	cag	tat	aca	aca	1765
148	Lys	Gly	Gly	Tyr	Lys	Asn	Trp	Phe	Leu	Cys	Tyr	Ser	Gln	Tyr	Thr	Thr	
149					270				275							280	
151	aat	gct	aag	gtc	act	cca	ccc	cca	caa	cac	cag	aat	gaa	gag	ttg	tct	1813
152	Asn	Ala	Lys	Val	Thr	Pro	Pro	Pro	Gln	His	Gln	Asn	Glu	Glu	Leu	Ser	
153					285				290							295	
155	atc	tca	ttg	gat	ttt	act	tat	ccc	tca	ttg	gaa	gaa	tca	att	cct	tct	1861
156	Ile	Ser	Leu	Asp	Phe	Thr	Tyr	Pro	Ser	Leu	Glu	Glu	Ser	Ile	Pro	Ser	
157					300				305							310	
159	aaa	cct	gct	gcc	gag	atg	cca	cct	cca	cct	ata	aaa	gtg	gat	gaa	gac	1909
160	Lys	Pro	Ala	Ala	Glu	Met	Pro	Pro	Pro	Pro	Ile	Lys	Val	Asp	Glu	Asp	
161					315				320							325	
163	ata	gaa	ttg	ata	agt	gat	caa	ata	agt	gat	aat	gat	caa	aat	gag	agg	1957
164	Ile	Glu	Leu	Ile	Ser	Asp	Gln	Ile	Ser	Asp	Asn	Asp	Gln	Asn	Glu	Arg	
165					330				335							345	
167	aca	gga	cca	ctg	aat	ata	tca	att	cca	gtt	gaa	tca	gtt	gct	gct	tct	2005
168	Thr	Gly	Pro	Leu	Asn	Ile	Ser	Ile	Pro	Val	Glu	Ser	Val	Ala	Ala	Ser	
169					350				355							360	
171	aaa	tct	gat	gtt	tca	ccc	atc	att	cag	cca	gtg	cct	agc	ata	aag	aat	2053
172	Lys	Ser	Asp	Val	Ser	Pro	Ile	Ile	Gln	Pro	Val	Pro	Ser	Ile	Lys	Asn	
173					365				370							375	
175	gtt	cca	cag	att	gat	cat	act	aaa	aaa	ctg	gca	gtc	aaa	ttg	cct	gaa	2101
176	Val	Pro	Gln	Ile	Asp	His	Thr	Lys	Lys	Leu	Ala	Val	Lys	Leu	Pro	Glu	
177					380				385							390	
179	gag	cat	ata	atc	aaa	tct	gaa	agt	aca	aat	cat	gag	caa	cag	tct	cct	2149
180	Glu	His	Ile	Ile	Lys	Ser	Glu	Ser	Thr	Asn	His	Glu	Gln	Gln	Ser	Pro	
181					395				400							405	
183	cag	aat	gaa	aaa	gtt	att	cct	gat	tgt	tcc	acc	aag	cca	qta	gtt	tcc	2197
184	Gln	Asn	Glu	Lys	Val	Ile	Pro	Asp	Cys	Ser	Thr	Lys	Pro	Val	Val	Ser	
185					410				415							425	
187	tct	cca	act	ctc	atg	tta	aca	gat	gaa	aag	gct	cat	att	cat	gca		2245
188	Ser	Pro	Thr	Leu	Met	Leu	Thr	Asp	Glu	Glu	Lys	Ala	His	Ile	His	Ala	
189					430				435							440	
191	gaa	act	gct	ctt	cta	atg	gag	aaa	aac	aaa	caa	gaa	aaa	gaa	ctt	cag	2293
192	Glu	Thr	Ala	Leu	Leu	Met	Glu	Lys	Asn	Lys	Gln	Glu	Lys	Glu	Leu	Gln	
193					445				450							455	
195	gaa	aga	cag	caa	ggg	aaa	cag	aaa	gaa	act	gag	gag	gga	aga	aca	cga	2341
196	Glu	Arg	Gln	Gln	Gly	Lys	Gln	Lys	Glu	Thr	Glu	Glu	Gly	Arg	Thr	Arg	
197					460				465							470	
199	gca	aaa	agc	caa	aaa	gaa	aca	aga	agc	tga	agaaaaatgaa	attacacaga					2391
200	Ala	Lys	Ser	Gln	Lys	Glu	Thr	Arg	Ser								

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203	agcaacaaaa	agcaaaagaa	gaaatggaga	agaaagaacg	tgaacaggcc	aagaaagagg	2451
205	ataaagaaat	ctcagcaaag	aaggcCAAAG	aaataacaag	agtaaaaaga	caaagtaaaa	2511
207	gtgatcatga	aacctctgg	gcccagaag	ctgtagagga	cagggggaga	agatgttcaa	2571
209	ccccagaagt	acagaaaaag	tcaacaagag	atgtgtccc	tacatctgc	acaggggatt	2631
211	caggttcagg	caagccttt	aagattaaag	gacaaccaga	aactggaatt	ctaaggacag	2691
213	aaacttttag	agaggataca	gatgatactt	aaagaaataa	aactcaacga	gaaccttcga	2751
215	taatagcacg	aagtgaagaa	atggggagga	tggtaccagg	actgccttca	ggctgggcca	2811
217	agtttcttga	tccaaatcact	gaaacgtt	attattatca	ttcaccacta	acactgttca	2871
219	tatgtaccca	ctggaaatgg	cttccttc	tgcacccct	tccacccctc	caactcataa	2931
221	aggcaagcca	cagattcctg	ctaagcagga	taggaacct	tccaaactga	aatgctctt	2991
223	ctcctcccc	gatataaccc	aggctattca	agaggaagcc	agcagtaact	ccaacagtt	3051
225	atcaggaaga	caagccaaca	tgctaccct	aagctgagat	ctcaaggc	tctgcttctc	3111
227	agatttggaa	actcaatcct	gttttggag	gtctggacc	agcttctact	ggacttcgta	3171
229	acttaggaaa	tacttggat	atgaactcaa	tattgcagt	cctatgtat	cctccacatt	3231
231	tggctgatta	tttcaaccga	aactgtt	aggatgat	taacaagtc	aatttggtag	3291
233	gggcataaaag	gtgaagtggc	agaagaattt	ggtataatca	tgaagcccc	gtggacagga	3351
235	cagtatagat	atatcagtcc	aaaagacctt	aaagtcacca	ttgggaagat	caattaccag	3411
237	tttgcaggat	acagtcaaga	ttcacaagaa	tttcttctgt	tcctaatgg	ttggctccat	3471
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241	aatgacttta	aagctgcaga	acatgcctgg	cagaaacaca	agcggctcta	tgagtctatt	3591
243	attgtgcac	ttttcaggg	tcaattcaa	tctacagtac	agtcctc	ccgtcacaaa	3651
245	aagtcttagga	cacttgaggc	cttcatgtat	ttgtctctac	tgatagcatc	cacaagtaaa	3711
247	tgtacattat	aggattgc	tagattatt	tctaaagaag	aaaaactcat	agataataac	3771
249	agattttact	gcaatctt	cagagctcg	cgggattctt	aaaaaagaaa	tctggaagtt	3831
251	accacctgt	cttttagtgc	atctgaaaca	ttttcttac	aatggcaggt	ggaaacaaaa	3891
253	attacagaca	tctgtggact	tcccgtttaga	aaatcttgc	ttgtcacagt	atgttattgg	3951
255	tccaaagaac	aatttgaaga	aatataattt	gttttctgtt	tca	gccccgtt	4011
257	ggatggaggc	cattacacag	cctactgt	aaatgcagca	aaacagcggt	ggtttaagtt	4071
259	tgtatgtat	gaagttctg	atatctctgt	ttcttctgt	aatcttc	cgacttat	4131
261	cctctttat	actccttgg	gaccatgagt	aactgatgt	ggcacataa	gagacatagg	4191
263	ttataaaacta	gttatcttt	aaaaggctca	gcaacacaat	tcttgaat	cttatcaaga	4251
265	taggttgc	aatagctggc	catttagagg	aattcttag	cagtggagc	tgttacta	4311
267	gcactatata	attcctgtca	gtggtgacaa	ataacactt	acaagtattt	cagtaagcat	4371
269	cacttacagg	taccattat	ttcaaaacaa	cttttttagt	ctgctccaa	gttaaaataa	4431
271	ttaacttagct	aagcattatt	attctactgg	tctaaaacc	tttgtaccc	tttttcctt	4491
273	ttcactgtt	cagccctt	acatttctaa	atcccattt	cataactat	gaatactcta	4551
275	gaatgatgt	aagcagatag	gaatgtatgt	gtacatattt	attgcatact	tacacatcaa	4611
277	atcgatatac	atagttaac	atgtggct	ttcgtaaaac	ttagaaact	gaggattgca	4671
279	ttttttctt	tgagcatatt	ttgagtaact	gcagtctt	cttagggaaa	tgacagggca	4731
281	aagctat	tctgtggct	ttgggggc	taaatctt	tctt	aaaaaaa	4791
283	taaatggaaa	cttcctt	ttttttaaa	tgagacatta	aaatcttaat	gagaaaaatt	4851
285	taaaaagctc	aatatcact	ctcattagag	aaatgtaaat	caaagccaca	atgagatacc	4911
287	atctcccacc	agtcagaat	gtaattat	aaaagtcaag	aaacaataga	tgctggtag	4971
289	gctgtggaga	aataggaaca	cttttacact	gttgggg	atgtaaacta	gttcaaccat	5031
291	tgtggaaagac	agtgtggcc	ttcctcagag	atctagaacc	agaaatacta	tttgaccctt	5091
293	tgggtatcta	cccaaggaa	tataaatcat	tctactataa	agacacatgc	acacgtatgt	5151
295	ttactgcacg	actattaca	atagcaaaga	cttgaacca	acccaaatgt	ccatcagtga	5211
297	tagatggata	aagaaaatgt	ggtgcatacc	accatggat	agtacacac	cagaaaaagg	5271

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303	atgacaaacac	atggacacag	ggagggggaaac	aacacatatc	agggccttt	ggggagtgtg	5451
305	gggggcaagg	gacgagaact	tagaggatgg	gtcaataggt	gcagcaaacc	accatggcag	5511
307	actatacgc	tgtaacaaac	ctgcagggtc	tgcacatgt	tccttggaaacc	taaagtaaaa	5571
309	taaaacaaaag	caaattaaaa	aaagaaagcc	catgtcttac	atgtatgtat	atgttcattt	5631
311	cagcacttatt	cacaatagca	aagacatgg	atcaacctaa	atgtccatca	atggtagact	5691
313	ggataaaagaa	aatgtggcaa	atatgctcta	ccggcaggat	ttgatggcgt	gatgtctcac	5751
315	agaaaagttct	ccactcccg	acatgggtcc	ctcgcttcc	tgccttggaa	gcacagcagc	5811
317	aggcatcgtg	ggaaggtgaa	gagttccct	aaggatgacc	catccaagcc	ggtccacctc	5871
319	acagccttcc	tgggatacaa	gcgtggcatg	accacatcg	tgccggaaagt	cgacaggcca	5931
321	ggatccaagg	tgaacaagaa	ggaggtgggt	gaggctgtga	ccattgtgga	gaggccacca	5991
323	gtgggcattt	tgggctgcgt	ggaaacccct	caaggcttcc	ggacttgcaa	gactgtcttc	6051
325	gtcgagcaca	tcagtgatga	atgcaagagg	cgtttctata	agaactggca	taaatctaag	6111
327	aagaaggcct	ttaccaagta	ctgcaagaaa	tggcaggatg	aggatggcaa	gaagcagctg	6171
329	gagaaggact	tcagcagcat	gaagaagtac	tgccaagtca	tctgcgtcat	tgcccacacc	6231
331	cagatgcacc	tgcttcctct	gtgccagaag	aaggcccacc	tgatggagat	ccaggtgaat	6291
333	ggaggcactg	tggctgagaa	gctggactgg	gctggcaga	ggctcaagca	ccaggtacct	6351
335	gtgaaccaag	tgtttggca	gatgagatg	atcgacgtca	tcaggggtgac	caagggcaaa	6411
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339	ggcctgtgca	aggtggcctg	tattggggca	tggcatctg	ctcggtggg	cttctctgtg	6531
341	gtacgtgggt	ggcagaaaagg	ctaccatcac	cgcactgaga	tcaacaagat	ctataggatt	6591
343	ggctagggct	accttatcaa	gatggcaag	ctgatcaaga	acaatgcctc	cactgactat	6651
345	gacctgtctg	acaagagcat	caacccttgc	ggtggcttcg	tccactatgg	tgaagtgacc	6711
347	aatgactttt	tcatgtgaa	aggctgtgtg	gtggaaacca	agaagtgggt	gctcaccctc	6771
349	cacaagtcc	tgctgtgca	gacaaagcag	cgggtctgg	agaagatga	ccttaagttc	6831
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353	ttcatgggac	cactcaagaa	agaccgaatt	gcaaaggaag	aaggagctt	atgctggaa	6951
355	cagatattgc	aactgggggg	atctcaataa	aagttattt	ccattaaaaaa	aaaaagaaaa	7011
357	agaaaatgtg	gcacatatac	accacagaat	accatgcagc	cataaaaaaaag	aatgagatca	7071
359	tgtccttgc	aggaacatgg	atggagttgg	aggcattat	ccttagcaaa	ctgaggcagg	7131
361	aacagaaaac	caattaccac	atgttctcac	ttataagtat	gagttatatg	atgagaacac	7191
363	atggacacac	agaagggaaac	aacacacact	ggggtccact	tgagggtaga	gggtgggagg	7251
365	agggagagg						7260

368 <210> SEQ ID NO: 2  
369 <211> LENGTH: 1449  
370 <212> TYPE: DNA

371 <213> ORGANISM: Homo sapiens

373 <220> FEATURE:

374 <221> NAME/KEY: CDS

375 <222> LOCATION: (1)..(1449)

376 <223> OTHER INFORMATION:

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381 <223> OTHER INFORMATION: exon 1

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385 <221> NAME/KEY: misc\_feature

386 <222> LOCATION: (168)..(796)

RAW SEQUENCE LISTING ERROR SUMMARY  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30  
Seq#:31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,57,58,59  
Seq#:60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79

**VERIFICATION SUMMARY**  
PATENT APPLICATION: US/10/570,121

DATE: 11/17/2006  
TIME: 08:38:13

Input Set : F:\ARS-125-SEQ LIST.txt  
Output Set: N:\CRF4\11172006\J570121.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:35 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27  
L:46 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:38  
L:384 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:376  
L:1523 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:52,Line#:1516  
L:1871 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:55,Line#:1869